Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

Claim 1. (Withdrawn) A zinc finger polypeptide which binds to a target DNA sequence containing a modified base but not to an identical sequence containing the equivalent unmodified base.

Claim 2. (Withdrawn) A polypeptide according to claim 1, wherein the target DNA sequence comprises a triplet having 5-meC at the central position, and binding to the 5-meC residue by an α-helical zinc finger binding motif in the polypeptide is achieved by placing an Ala residue at position +3 of the α-helix of the zinc finger.

Claim 3. (Previously presented) A method for binding a DNA binding polypeptide of the Cys2 His2 zinc finger class to a DNA triplet in a target DNA sequence comprising 5-meC as the central residue in the target DNA triplet, the method comprising preparing a DNA binding polypeptide of the Cys2 His2 zinc finger class to bind to the DNA triplet, wherein binding to the 5-meC residue by an α-helical zinc finger DNA binding motif of the polypeptide is achieved by placing an Ala residue at position +3 of the α-helix of the zinc finger, and exposing the DNA binding polypeptide to the target DNA sequence, whereby the DNA binding polypeptide binds to the target DNA sequence.

Claim 4. (Currently amended) A method for binding a DNA binding polypeptide of the Cys2 His2 zinc finger class to a DNA triplet in target DNA sequence comprising 5-meC, but not to an identical triplet comprising unmethylated C, the method comprising preparing a DNA binding polypeptide of the Cys2 His2 zinc finger class to bind to the triplet comprising 5-meC, wherein binding to each base of the triplet by an α-helical zinc finger DNA binding motif in the polypeptide is determined as follows:

a) if the 5' base in the triplet is G, then position +6 in the α-helix is Arg or position ++2 is Asp, or position +6 in the α-helix is Arg and position ++2 is Asp;

b) if the 5' base in the triplet is A, then position +6 in the α-helix is Gln or Glu and ++2 is not Asp;

c) if the 5' base in the triplet is T, then position +6 in the α-helix is Ser or Thr and position ++2 is Asp; or position +6 is a hydrophobic amino acid other than Ala;

d) if the 5' base in the triplet is C, then position +6 in the α-helix is any amino acid, provided that position ++2 in the α-helix is not Asp;

e) ~~if the central base in the triplet is 5-meC, then~~ position +3 in the α-helix is Ala;

f) if the 3' base in the triplet is G, then position -1 in the α-helix is Arg;

g) if the 3' base in the triplet is A, then position -1 in the α- helix is Gln and position +2 is Ala;

h) if the 3' base in the triplet is T, then position -1 in the α-helix is Asn; or position -1 is Gln and position +2 is Ser;

i) if the 3' base in the triplet is C, then position -1 in the α-helix is Asp and Position +1 is Arg; and

exposing the DNA binding polypeptide to the target DNA sequence, whereby the DNA binding polypeptide binds to the target DNA sequence.

Claim 5. (Withdrawn) A method for producing a zinc finger polypeptide capable of binding to a DNA sequence comprising a modified residue, but not to an identical sequence comprising an equivalent unmodified residue, comprising the steps of:

a) providing a DNA library encoding a repertoire of zinc finger polypeptides, the DNA members of the library being at least partially randomized at one or more of the positions encoding residues -1, 2, 3 and 6 of an a-helical zinc finger binding motif of the zinc finger polypeptides;

b) displaying the library in a selection system and screening it against a target DNA sequence comprising the modified residue;

c) isolating the DNA members of the library encoding zinc finger polypeptides capable of binding to the target sequence; and

d) optionally, verifying that the zinc finger polypeptides do not bind significantly to a DNA sequence identical to the target DNA sequence but containing the equivalent unmodified residue in place of the modified residue.

Claim 6. (Withdrawn) A method according to claim 5, wherein the nucleic acid library encodes a repertoire of zinc finger polypeptides each possessing more than one zinc fingers, the nucleic acid members of the library being at least partially randomized at one or more of the positions encoding residues -1, 2, 3 and 6 of the α-helix in a zinc finger and at one or more of the positions encoding residues -1, 2, 3 and 6 of the α-helix in a further zinc finger of the zinc finger polypeptides.

Claim 7. (Withdrawn) The method according to claim 5 or claim 6, wherein the modified residue is 5-meC and the unmodified residue is C.

Claim 8. (Withdrawn) The method according to claim 5 or claim 6, wherein the modified residue is U and the unmodified residue is T.

Claim 9. (Withdrawn) The method according to claim 5 or claim 6, wherein the library is screened by phage display.

Claim 10. (Withdrawn) The method according to claim 6, wherein each zinc finger has the primary structure of (SEQ ID NO.:40):

X^a C X_{2-4} C X_{2-3} F X^c X X X X L X X H X X X^b H-linker

-1 1 2 3 4 5 6 7 8 9

wherein each of X, X^a, X^b and X^c is any amino acid, and

wherein X_{2-4} means either 2 or 4 amino acids are present at this position, and X_{2-3} means either 2 or 3 amino acids are present at this position.

Claim 11. (Withdrawn) The method according to claim 10, wherein X^a is $^F/_Y$-X or P-$^F/_Y$-X.

Claim 12. (Withdrawn) The method according to claim 10 or claim 11, wherein X_{2-4} is selected from the group consisting of S-X, E-X, K-X, T-X, P-X and R-X.

Claim 13. (Withdrawn) The method according to claim 10, wherein X^b is T or I.

Claim 14. (Withdrawn) The method according to claim 10, wherein X_{2-3} is selected from the group consisting of G-K-A, G-K-C, G-K-S, G-K-G, M-R-N and M-R.

Claim 15. (Withdrawn) The method according to claim 10, wherein the linker is the sequence set forth in SEQ ID NO.:41 or the sequence set forth in SEQ ID NO.:3.

Claim 16. (Withdrawn) The method according to claim 10, wherein position +9 is R or K.

Claim 17. (Withdrawn) The method according to claim 10, wherein positions +1, +5 and +8 are not occupied by any of hydrophobic amino acids F, W or Y.

Claim 18. (Withdrawn) The method according to claim 17, wherein positions +1, +5 and +8 are occupied by residues K, T and Q respectively.

Claim 19. (Withdrawn) The method of claim 3 or 4, wherein the preparing step comprises:

a) selecting a model zinc finger domain from the group consisting of naturally occurring zinc fingers and consensus zinc fingers; and

b) mutating the finger to introduce the Ala residue at position +3.

Claims 20. (Withdrawn) The method according to claim 19, wherein the model zinc finger is a consensus zinc finger whose structure is selected from the group consisting of the consensus structure set forth by SEQ ID NO.:1 and the consensus structure set forth by SEQ ID NO.:2.

Claim 21. (Withdrawn) The method according to claim 19 wherein the model zinc finger domain is a naturally occurring zinc finger whose structure is selected from one finger of a protein selected from the group consisting of Zif 268, GLI, Tramtrack, and YY1.

Claim 22. (Withdrawn) The method according to claim 21, wherein the model zinc finger is finger 2 of Zif 268.

Claim 23. (Previously presented) The method according to claim 3 or 4, wherein the binding protein comprises two or more zinc finger binding motifs.

Claim 24. (Withdrawn) The method according to claim 22, wherein the N-terminal zinc finger is preceded by a leader peptide having the sequence of SEQ ID NO.:39.

Claim 25. (Previously presented) The method according to claim 23, wherein the DNA binding protein is constructed by recombinant DNA technology, the method comprising the steps of:

a) preparing a DNA coding sequence encoding two or more zinc finger binding motifs;

b) inserting the DNA sequence into a suitable expression vector; and

c) expressing the DNA sequence in a host organism in order to obtain the DNA binding protein.

Claim 26. (Previously presented) The method according to claim 3 or 4 further comprising the steps of subjecting the DNA binding protein to one or more rounds of randomization and screening in order to improve the binding characteristics thereof.

Claim 27. (Withdrawn) A zinc finger polypeptide which binds to a target DNA sequence containing a modified base but does not bind to an identical sequence containing the equivalent unmodified base, preparable by a method according to any one of claims 3, 4 or 5.

Claim 28. (Previously presented) The method of either of claims 3 or 4, further comprising detecting the DNA binding polypeptide binding to the target DNA sequence.

Claim 29. (Previously presented) The method of either of claims 3 or 4, wherein the binding of the DNA binding polypeptide to the target DNA sequence regulates transcription of a gene.